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cont

9. (Amended) Method according to claim 1, characterized in that the third databank is the UNIGENE databank.

11. (Amended) Method according to claim 1, characterized in that further databanks are searched for linking members to the citation determined in the third databank, and addition of the corresponding further information or of references to the further information to the corresponding species sequences of increased importance.

12. (Amended) Method according to claim 1, characterized in that at least the second databank is a databank accessible to the public.

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13. (Amended) Method according to claim 5, characterized in that the further databanks are chosen from the group consisting of the Unigene, Genemap and GDB (new) and OMIM, KEGG and UMLS databanks.

14. (Amended) Method according to claim 1, characterized in that the addition of further information to the species sequences determined according to step f is carried out in a pipeline method, the information added being in the form of linking members to the assigned positions in further databanks.

15. (Amended) Method according to claim 1, characterized in that the species of interest is the human species, and in that the assigned group of biosequences comprises the biosequences of invertebrate animals, mammals, primates, rodents and vertebrates, and the not yet classified new entries of the second databank.
